

10/02/02



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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/083,641A

DATE: 10/02/2002
TIME: 15:26:57

Input Set : A:\Seq Listing #2.txt
Output Set: N:\CRF4\10022002\J083641A.raw

3 <110> APPLICANT: HAYSTEAD, TIMOTHY A
 5 <120> TITLE OF INVENTION: SMOOTH MUSCLE MYOSIN PHOSPHATASE ASSOCIATED KINASE
 7 <130> FILE REFERENCE: 1579-647
 9 <140> CURRENT APPLICATION NUMBER: 10/083,641A
 10 <141> CURRENT FILING DATE: 2002-02-27
 12 <150> PRIOR APPLICATION NUMBER: 60/271,436
 13 <151> PRIOR FILING DATE: 2001-02-27
 15 <160> NUMBER OF SEQ ID NOS: 17
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 15
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Description of Artificial Sequence: Endogenous kinase
 26 copurifies with SMPP-1M
 28 <400> SEQUENCE: 1
 29 Lys Lys Lys Arg Gln Ser Arg Arg Ser Thr Gln Gly Val Thr Leu
 30 1 5 10 15
 33 <210> SEQ ID NO: 2
 34 <211> LENGTH: 13
 35 <212> TYPE: PRT
 36 <213> ORGANISM: Artificial Sequence
 38 <220> FEATURE:
 39 <223> OTHER INFORMATION: Description of Artificial Sequence: human pDAPK3
 41 <400> SEQUENCE: 2
 42 Met Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val
 43 1 5 10
 46 <210> SEQ ID NO: 3
 47 <211> LENGTH: 320
 48 <212> TYPE: PRT
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: Description of Artificial Sequence: ZIP Kinase
 54 <400> SEQUENCE: 3
 55 Met Ser Thr Phe Arg Gln Glu Asp Val Glu Asp His Tyr Glu Met Gly
 56 1 5 10 15
 58 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Arg Lys Cys Arg Gln
 59 20 25 30
 61 Lys Gly Thr Gly Lys Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg
 62 35 40 45
 64 Leu Pro Ser Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
 65 50 55 60

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67 Val Asn Ile Leu Arg Glu Ile Arg His Pro Asn Ile Ile Thr Leu His
68 65 70 75 80
70 Asp Ile Phe Glu Asn Lys Thr Asp Val Val Leu Ile Leu Glu Leu Val
71 85 90 95
73 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr
74 100 105 110
76 Glu Asp Glu Ala Thr Gln Phe Leu Lys Gln Ile Leu Asp Gly Val His
77 115 120 125
79 Tyr Leu His Ser Lys Arg Ile Ala His Phe Asp Leu Lys Pro Glu Asn
80 130 135 140
82 Ile Met Leu Leu Asp Lys Asn Val Pro Asn Pro Arg Ile Lys Leu Ile
83 145 150 155 160
85 Asp Phe Gly Ile Ala His Lys Ile Glu Ala Gly Asn Glu Phe Lys Asn
86 165 170 175
88 Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
89 180 185 190
91 Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
92 195 200 205
94 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Glu Thr Lys Gln Glu
95 210 215 220
97 Thr Leu Thr Asn Ile Ser Ala Val Asn Tyr Asp Phe Asp Glu Glu Tyr
98 225 230 235 240
100 Phe Ser Ser Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu
101 245 250 255
103 Val Lys Asp Pro Lys Arg Arg Met Thr Ile Ala Gln Ser Leu Glu His
104 260 265 270
106 Ser Trp Ile Lys Val Arg Arg Arg Glu Asp Gly Ala Arg Lys Pro Glu
107 275 280 285
109 Arg Arg Arg Leu Arg Ala Ala Arg Leu Arg Glu Tyr Ser Leu Lys Ser
110 290 295 300
112 His Ser Ser Met Pro Arg Asn Thr Ser Tyr Ala Ser Phe Glu Arg Phe
113 305 310 315 320

119 <210> SEQ ID NO: 4

120 <211> LENGTH: 13

121 <212> TYPE: PRT

122 <213> ORGANISM: Artificial Sequence

124 <220> FEATURE:

125 <223> OTHER INFORMATION: Description of Artificial Sequence: rat DAP-like kinase

127 <220> FEATURE:

128 <221> NAME/KEY: Unsure

129 <222> LOCATION: (6), (9)

130 <223> OTHER INFORMATION: Xaa can be any amino acid

132 <400> SEQUENCE: 4

W--> 133 Met Leu Leu Asp Lys Xaa Ile Phe Xaa Arg Pro Ile Gln

134 1 5 10

137 <210> SEQ ID NO: 5

138 <211> LENGTH: 13

139 <212> TYPE: PRT

140 <213> ORGANISM: Artificial Sequence

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142 <220> FEATURE:
143 <223> OTHER INFORMATION: Description of Artificial Sequence: D-glycerate dehydrogenase
145 <220> FEATURE:
146 <221> NAME/KEY: Unsure
147 <222> LOCATION: (8), (10), (11) and (13)
148 <223> OTHER INFORMATION: Xaa can be any amino acid
150 <400> SEQUENCE: 5
W--> 151 Met Thr Ile Ala Gln Asn Leu Xaa Tyr Xaa Xaa Ile Xaa
152 1 5 10
155 <210> SEQ ID NO: 6
156 <211> LENGTH: 1093
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Description of Artificial Sequence: Putative nucleotide sequence of smooth muscle MYPT-Kinase
162
164 <220> FEATURE:
165 <221> NAME/KEY: Unsure
166 <222> LOCATION: (2), (7), (37), (39), (1056), (1081) and (1092)
167 <223> OTHER INFORMATION: N can be A, C, G or T
169 <400> SEQUENCE: 6
W--> 170 gntatgnata tcgggttaat cggccggagc tcgcccncng ggcagctgga ctccctctca 60
171 gacctccttc tttctcgccc tcagcacggg attaacctca cttgactgtt cttgggtccc 120
172 cgggtccggg ccagcgtcct ctccctcaag gcaatccccca agtgtctgtc atgaggctct 180
173 ttgggcagtt ctgttgttgt gggaaacctg ggaacagatg cacagaggtt gggcacaga 240
174 gtcctgcctt cctctgggtc tgcagcgtt agctgttcct tcccccacag cggccagttc 300
175 gccatcgtgc gcaagtgcga gcagaagggc accggcatgg agtacgcggc caagttcata 360
176 aagaagcggc gcctgcccgc cagccggcgc ggtgtgagcc gtgaggagat cgagcgcgag 420
177 gtgagcatcc tgcgcgagat cgcgcacccc aacatcatca cgctgcacga tgggttcgag 480
178 aacaagacag atgtggtgct gatcttggag ctgggtgtccg gggcgact tttcgacttt 540
179 ctggctgaga aggtacactg acagaggatg aggccacgcgca gttcctcaag cagatcctgg 600
180 acgggtgtcca ctacctgcac tccaagcgcgca tcgcgcactt tgacactgaag ccggagaaca 660
181 tcatgttgcg gacaagcat gcagccagcc cacgcattaa gctcatcgac tttggcatcg 720
182 cgcacaggat cgaggccggt agcgagttca agaacatctt tggcacgcga gagttcgctg 780
183 gtgaggggca ggtgtggca ccacccgata gggtagattt tgacacggct tggctgacc 840
184 tgcctcaaca atcctgtctt ccacagcccc tgagattgtt aactatgaac cacttggctt 900
185 ggaagctgat atgtggagca tcggcgtcat cacotacatc ctgtgagttc ctgagatggg 960
186 caggggcctc agactgtacc tgctagaggc ccaggatca gggctggcac ctctgcaaac 1020
W--> 187 tgcaaacact ggggctgaga gatgtccctg ggaacnctgg atatgcctgg gccccaccaa 1080
W--> 188 ngtaggacca tnc 1093
191 <210> SEQ ID NO: 7
192 <211> LENGTH: 34
193 <212> TYPE: PRT
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino acid sequence of rat aorta smooth muscle MYPT-kinase
198
200 <220> FEATURE:
201 <221> NAME/KEY: Unsure

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202 <222> LOCATION: (1), (3) and (13)

203 <223> OTHER INFORMATION: Xaa can be any amino acid

205 <400> SEQUENCE: 7

W--> 206 Xaa Met Xaa Ile Gly Leu Ile Gly Arg Ser Ser Pro Xaa Gly Gln Leu

207 1 5 10 15

209 Asp Ser Leu Ser Asp Leu Leu Leu Ser Arg Pro Gln His Gly Ile Asn

210 20 25 30

212 Leu Thr

216 <210> SEQ ID NO: 8

217 <211> LENGTH: 22

218 <212> TYPE: PRT

219 <213> ORGANISM: Artificial Sequence

221 <220> FEATURE:

222 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino acid sequence of rat

223 aorta smooth muscle MYPT-kinase

225 <400> SEQUENCE: 8

226 Leu Phe Leu Gly Pro Arg Cys Arg Ala Ser Val Leu Ser Leu Lys Ala

227 1 5 10 15

229 Ile Pro Lys Cys Leu Ser

230 20

233 <210> SEQ ID NO: 9

234 <211> LENGTH: 125

235 <212> TYPE: PRT

236 <213> ORGANISM: Artificial Sequence

238 <220> FEATURE:

239 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino acid sequence of rat

240 aorta smooth muscle MYPT-kinase

242 <400> SEQUENCE: 9

243 Gly Ser Leu Gly Ser Ser Val Val Val Gly Asn Leu Gly Thr Asp Ala

244 1 5 10 15

246 Gln Arg Leu Gly Tyr Arg Val Leu Pro Ser Ser Gly Ser Ala Ala Leu

247 20 25 30

249 Ser Cys Ser Phe Pro His Ser Gly Phe Ala Ile Val Arg Lys Cys Lys

250 35 40 45

252 Gly Thr Gly Met Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg Leu

253 50 55 60

255 Pro Ser Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu Val

256 65 70 75 80

258 Ser Ile Leu Arg Glu Ile Arg His Pro Asn Ile Ile Thr Leu His Asp

259 85 90 95

261 Val Phe Glu Asn Lys Thr Asp Val Val Leu Ile Leu Glu Leu Val Ser

262 100 105 110

264 Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys Asp His

265 115 120 125

268 <210> SEQ ID NO: 10

269 <211> LENGTH: 28

270 <212> TYPE: PRT

271 <213> ORGANISM: Artificial Sequence

273 <220> FEATURE:

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Input Set : A:\Seq Listing #2.txt
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274 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino
275 acid sequence of rat aorta smooth muscle
276 MYPT-kinase
278 <400> SEQUENCE: 10
279 Gln Arg Met Arg Pro Arg Ser Ser Ser Arg Ser Trp Thr Val Ser
280 1 5 10 15
282 Thr Thr Cys Thr Pro Ser Ala Ser Arg Thr Leu Thr
283 20 25
286 <210> SEQ ID NO: 11
287 <211> LENGTH: 55
288 <212> TYPE: PRT
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino
293 acid sequence of rat aorta smooth muscle
294 MYPT-kinase
296 <400> SEQUENCE: 11
297 Ser Arg Arg Thr Ser Cys Cys Trp Thr Ser Met Gln Pro Ala His Ala
298 1 5 10 15
300 Leu Ser Ser Ser Thr Leu Ala Ser Arg Thr Gly Ser Arg Pro Val Ala
301 20 25 30
303 Ser Ser Arg Thr Ser Leu Ala Arg Gln Ser Ser Ser Val Arg Gly Arg
304 35 40 45
306 Cys Gly His His Pro Ile Gly
307 50 55
310 <210> SEQ ID NO: 12
311 <211> LENGTH: 18
312 <212> TYPE: PRT
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino
317 acid sequence of rat aorta smooth muscle
318 MYPT-kinase
320 <400> SEQUENCE: 12
321 Ile Leu His Gly Leu Gly Leu Thr Cys Leu Asn Asn Pro Val Phe His
322 1 5 10 15
324 Ser Pro
328 <210> SEQ ID NO: 13
329 <211> LENGTH: 4
330 <212> TYPE: PRT
331 <213> ORGANISM: Artificial Sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: Description of Artificial Sequence: Deduced amino
335 acid sequence of rat aorta smooth muscle
336 MYPT-kinase
338 <400> SEQUENCE: 13
339 Asp Cys Lys Leu
340 1
343 <210> SEQ ID NO: 14

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/083,641A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 6,9
Seq#:5; Xaa Pos. 8,10,11,13
Seq#:6; N Pos. 2,7,37,39,1056,1081,1092
Seq#:7; Xaa Pos. 1,3,13
Seq#:17; Xaa Pos. 15,18